

SEQUENCE LISTING

<110> Metanomics GmbH & Co. KGaA

<120> Process for preparing amino acids

<130> 2002_960

<140> PF54195

<141> 2002-12-20

<160> 26

<170> PatentIn version 3.1

<210> 1

<211> 1164

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1164)

<223> Threonine aldolase

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ttg cgg tca gac aca ttc acc act cca act gca gag atg atg gag gcc	96
Leu Arg Ser Asp Thr Phe Thr Thr Pro Thr Ala Glu Met Met Glu Ala	
20 25 30	

gct tta gag gcc tct atc ggt gac gct gtc tac ggt gaa gat gtt gac	144
Ala Leu Glu Ala Ser Ile Gly Asp Ala Val Tyr Gly Glu Asp Val Asp	
35 40 45	

acc gtt agg ctc gaa cag acc gtt gcc cgc atg gct ggc aaa gaa gca	192
Thr Val Arg Leu Glu Gln Thr Val Ala Arg Met Ala Gly Lys Glu Ala	
50 55 60	

ggt ttg ttc tgt gtc tct ggg act ttg tcc aac cag att gcc atc aga	240
Gly Leu Phe Cys Val Ser Gly Thr Leu Ser Asn Gln Ile Ala Ile Arg	
65 70 75 80	

act	cac	ttg	atg	caa	cct	cca	tac	tct	att	cta	tgt	gat	tac	agg	gct	288
Thr	His	Leu	Met	Gln	Pro	Pro	Tyr	Ser	Ile	Leu	Cys	Asp	Tyr	Arg	Ala	
				85					90					95		
cac	gtt	tac	act	cac	gaa	gcc	gct	gga	ctg	gcg	atc	ttg	tct	caa	gcg	336
His	Val	Tyr	Thr	His	Glu	Ala	Ala	Gly	Leu	Ala	Ile	Leu	Ser	Gln	Ala	
			100					105					110			
atg	gtg	gtt	cct	gtg	gtt	cct	tcc	aac	ggg	gac	tac	ttg	acc	ttg	gaa	384
Met	Val	Val	Pro	Val	Val	Pro	Ser	Asn	Gly	Asp	Tyr	Leu	Thr	Leu	Glu	
		115					120					125				
gac	atc	aag	tca	cac	tac	gtc	cca	gac	gac	ggg	gat	att	cac	ggg	gcc	432
Asp	Ile	Lys	Ser	His	Tyr	Val	Pro	Asp	Asp	Gly	Asp	Ile	His	Gly	Ala	
	130					135					140					
ccc	acc	aga	ttg	att	tct	ctg	gaa	aac	act	tta	cac	ggg	att	gtt	tat	480
Pro	Thr	Arg	Leu	Ile	Ser	Leu	Glu	Asn	Thr	Leu	His	Gly	Ile	Val	Tyr	
145					150					155					160	
cca	ttg	gaa	gaa	ctg	gtc	cgc	atc	aaa	gct	tgg	tgt	atg	gaa	aat	ggg	528
Pro	Leu	Glu	Glu	Leu	Val	Arg	Ile	Lys	Ala	Trp	Cys	Met	Glu	Asn	Gly	
			165						170					175		
ctc	aaa	cta	cat	tgt	gac	ggg	gcc	aga	atc	tgg	aat	gcc	gct	gca	caa	576
Leu	Lys	Leu	His	Cys	Asp	Gly	Ala	Arg	Ile	Trp	Asn	Ala	Ala	Ala	Gln	
			180					185						190		
tct	ggc	gtg	cca	tta	aag	caa	tat	ggg	gaa	atc	ttc	gac	tcc	atc	tcc	624
Ser	Gly	Val	Pro	Leu	Lys	Gln	Tyr	Gly	Glu	Ile	Phe	Asp	Ser	Ile	Ser	
		195					200					205				
atc	tgt	cta	tcc	aag	tct	atg	ggg	gct	cct	att	ggg	tcc	gtc	ttg	gtt	672
Ile	Cys	Leu	Ser	Lys	Ser	Met	Gly	Ala	Pro	Ile	Gly	Ser	Val	Leu	Val	
	210					215					220					
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Gly	Asn	Leu	Lys	Phe	Val	Lys	Lys	Ala	Thr	His	Phe	Arg	Lys	Gln	Gln	
225					230					235					240	
ggg	ggg	ggg	att	aga	caa	tct	ggg	atg	atg	gct	aga	atg	gct	ctt	gta	768
Gly	Gly	Gly	Ile	Arg	Gln	Ser	Gly	Met	Met	Ala	Arg	Met	Ala	Leu	Val	
				245				250						255		
aac	atc	aac	aac	gat	tgg	aag	tcc	caa	ttg	ctg	tac	tcg	cac	tct	ttg	816
Asn	Ile	Asn	Asn	Asp	Trp	Lys	Ser	Gln	Leu	Leu	Tyr	Ser	His	Ser	Leu	
			260					265						270		
gct	cat	gaa	tta	gcc	gaa	tat	tgt	gag	gca	aag	ggc	atc	ccg	cta	gag	864
Ala	His	Glu	Leu	Ala	Glu	Tyr	Cys	Glu	Ala	Lys	Gly	Ile	Pro	Leu	Glu	
		275					280					285				
tct	cca	gca	gac	acc	aac	ttt	gtc	ttt	att	aac	ctg	aag	gcc	gct	aga	912
Ser	Pro	Ala	Asp	Thr	Asn	Phe	Val	Phe	Ile	Asn	Leu	Lys	Ala	Ala	Arg	
	290					295					300					
atg	gac	cca	gat	gtc	ctt	gtt	aag	aag	ggg	ttg	aag	tac	aac	gtt	aag	960
Met	Asp	Pro	Asp	Val	Leu	Val	Lys	Lys	Gly	Leu	Lys	Tyr	Asn	Val	Lys	
305					310					315					320	
cta	atg	ggg	ggg	aga	gtc	tcg	ttc	cac	tat	caa	gtc	acc	aga	gat	act	1008
Leu	Met	Gly	Gly	Arg	Val	Ser	Phe	His	Tyr	Gln	Val	Thr	Arg	Asp	Thr	
				325					330					335		

ttg gaa aaa gtc aaa ttg gcc atc tcc gag gcc ttc gac tat gct aaa 1056
 Leu Glu Lys Val Lys Leu Ala Ile Ser Glu Ala Phe Asp Tyr Ala Lys
 340 345 350

gaa cat cct ttc gac tgt aac gga cct acc cag att tac cgt agt gaa 1104
 Glu His Pro Phe Asp Cys Asn Gly Pro Thr Gln Ile Tyr Arg Ser Glu
 355 360 365

tcc acc gag gtc gac gtt gat ggc aac gct atc cgc gaa ata aaa acc 1152
 Ser Thr Glu Val Asp Val Asp Gly Asn Ala Ile Arg Glu Ile Lys Thr
 370 375 380

tac aaa tac tga 1164
 Tyr Lys Tyr
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<210> 2
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 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 2

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 Ala Leu Glu Ala Ser Ile Gly Asp Ala Val Tyr Gly Glu Asp Val Asp
 35 40 45
 Thr Val Arg Leu Glu Gln Thr Val Ala Arg Met Ala Gly Lys Glu Ala
 50 55 60
 Gly Leu Phe Cys Val Ser Gly Thr Leu Ser Asn Gln Ile Ala Ile Arg
 65 70 75 80
 Thr His Leu Met Gln Pro Pro Tyr Ser Ile Leu Cys Asp Tyr Arg Ala
 85 90 95
 His Val Tyr Thr His Glu Ala Ala Gly Leu Ala Ile Leu Ser Gln Ala
 100 105 110
 Met Val Val Pro Val Val Pro Ser Asn Gly Asp Tyr Leu Thr Leu Glu
 115 120 125
 Asp Ile Lys Ser His Tyr Val Pro Asp Asp Gly Asp Ile His Gly Ala
 130 135 140
 Pro Thr Arg Leu Ile Ser Leu Glu Asn Thr Leu His Gly Ile Val Tyr
 145 150 155 160
 Pro Leu Glu Glu Leu Val Arg Ile Lys Ala Trp Cys Met Glu Asn Gly
 165 170 175
 Leu Lys Leu His Cys Asp Gly Ala Arg Ile Trp Asn Ala Ala Ala Gln
 180 185 190

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Ser Gly Val Pro Leu Lys Gln Tyr Gly Glu Ile Phe Asp Ser Ile Ser
195 200 205

Ile Cys Leu Ser Lys Ser Met Gly Ala Pro Ile Gly Ser Val Leu Val
210 215 220

Gly Asn Leu Lys Phe Val Lys Lys Ala Thr His Phe Arg Lys Gln Gln
225 230 235 240

Gly Gly Gly Ile Arg Gln Ser Gly Met Met Ala Arg Met Ala Leu Val
245 250 255

Asn Ile Asn Asn Asp Trp Lys Ser Gln Leu Leu Tyr Ser His Ser Leu
260 265 270

Ala His Glu Leu Ala Glu Tyr Cys Glu Ala Lys Gly Ile Pro Leu Glu
275 280 285

Ser Pro Ala Asp Thr Asn Phe Val Phe Ile Asn Leu Lys Ala Ala Arg
290 295 300

Met Asp Pro Asp Val Leu Val Lys Lys Gly Leu Lys Tyr Asn Val Lys
305 310 315 320

Leu Met Gly Gly Arg Val Ser Phe His Tyr Gln Val Thr Arg Asp Thr
325 330 335

Leu Glu Lys Val Lys Leu Ala Ile Ser Glu Ala Phe Asp Tyr Ala Lys
340 345 350

Glu His Pro Phe Asp Cys Asn Gly Pro Thr Gln Ile Tyr Arg Ser Glu
355 360 365

Ser Thr Glu Val Asp Val Asp Gly Asn Ala Ile Arg Glu Ile Lys Thr
370 375 380

Tyr Lys Tyr
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<211> 376
<212> PRT
<213> Canola

<400> 3

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20 25 30

Thr Glu Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp
35 40 45

Val Leu Gly Tyr Asp Pro Thr Ala Phe Arg Leu Glu Thr Glu Met Ala
50 55 60

Lys Thr Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met

65	70	75	80
Gly Asn Leu Val	Ser Val Leu Val	His Cys Asp Val	Arg Gly Ser Glu
	85	90	95
Val Ile Leu Gly	Asp Asn Cys His	Ile Asn Ile Phe	Glu Asn Gly Gly
	100	105	110
Ile Ala Thr Ile	Gly Gly Val His	Pro Arg Gln Val	Lys Asn Asn Asp
	115	120	125
Asp Gly Thr Met	Asp Ile Asp Leu	Ile Glu Ala Ala	Ile Arg Asp Pro
	130	135	140
Met Gly Glu Leu	Phe Tyr Pro Thr	Thr Lys Leu Ile	Cys Leu Glu Asn
	145	150	155
Thr His Ala Asn	Ser Gly Gly Arg	Cys Leu Ser Val	Glu Tyr Thr Asp
	165	170	175
Arg Val Gly Glu	Leu Ala Lys Lys	His Gly Leu Lys	Leu His Ile Asp
	180	185	190
Gly Ala Arg Ile	Phe Asn Ala Ser	Val Ala Leu Gly	Val Pro Val Asp
	195	200	205
Arg Leu Val Gln	Ala Ala Asp Ser	Val Ser Val Cys	Leu Ser Lys Gly
	210	215	220
Ile Gly Ala Pro	Val Gly Ser Val	Ile Val Gly Ser	Lys Asn Phe Ile
	225	230	235
Ala Lys Ala Arg	Arg Leu Arg Lys	Thr Leu Gly Gly	Gly Met Arg Gln
	245	250	255
Ile Gly Leu Leu	Cys Ala Ala Ala	Leu Val Ala Leu	Gln Glu Asn Val
	260	265	270
Gly Lys Leu Glu	Ser Asp His Lys	Lys Ala Arg Leu	Leu Ala Asp Gly
	275	280	285
Leu Asn Glu Val	Lys Gly Leu Arg	Val Asp Ala Cys	Ser Val Glu Thr
	290	295	300
Asn Met Val Phe	Ile Asp Ile Glu	Glu Gly Thr Lys	Thr Arg Ala Glu
	305	310	315
Lys Ile Cys Lys	Tyr Met Glu Glu	Arg Gly Ile Leu	Val Met Gln Glu
	325	330	335
Ser Ser Ser Arg	Met Arg Val Val	Leu His His Gln	Ile Ser Ala Ser
	340	345	350
Asp Val Gln Tyr	Ala Leu Ser Cys	Phe Gln Gln Ala	Leu Ala Val Lys
	355	360	365
Gly Val Gln Lys	Glu Met Gly Asn		
	370	375	

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<210> 4
 <211> 115
 <212> PRT
 <213> Soybean

<400> 4

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Leu Phe Gly Leu Leu Ala Ile Leu Leu Glu Tyr Leu Glu Lys Met Val
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Pro Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro Ser Glu
20           25           30
Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp Val Leu
35           40           45
Gly Arg Asp Pro Ser Cys Phe Arg Leu Glu Thr Glu Met Ala Lys Ile
50           55           60
Leu Gly Lys Glu Gly Ala Leu Phe Val Pro Ser Gly Thr Met Ala Asn
65           70           75           80
Leu Ile Ser Val Leu Val His Cys Asp Ile Arg Gly Ser Glu Val Ile
85           90           95
Leu Gly Asp Asn Ser His Ile His Ile Tyr Glu Asn Gly Gly Ile Ala
100          105          110
Thr Leu Gly
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<210> 5
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 <213> Rice

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<221> misc_feature

<222> (1)..(127)

<223> unknown or other

<400> 5

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Ala Leu Val Ala Leu Gln Glu Asn Val Gly Lys Leu Gln Ser Asp His
20           25           30
Asn Lys Ala Lys Leu Leu Ala Asp Gly Leu Asn Glu Ile Lys Gly Leu
35           40           45

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Arg Val Asp Ile Ser Ser Val Glu Thr Asn Ile Ile Tyr Val Glu Val
 50 55 60

Glu Glu Gly Ser Arg Ala Thr Ala Ala Lys Leu Cys Lys Asp Leu Glu
 65 70 75 80

Asp Tyr Gly Ile Leu Leu Met Pro Met Gly Ser Ser Arg Leu Arg Ile
 85 90 95

Val Phe His His Gln Ile Ser Ala Ser Asp Val Gln Tyr Ala Leu Ser
 100 105 110

Cys Phe Gln Gln Ala Val Asn Gly Val Arg Asn Glu Asn Gly Asn
 115 120 125

<210> 6
 <211> 147
 <212> PRT
 <213> Rice

<400> 6

Gly Arg Arg Phe Arg Ala Ile Arg Asp Pro Met Gly Glu Leu Phe Tyr
 1 5 10 15

Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn Thr His Ala Asn Ser Gly
 20 25 30

Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp Arg Val Gly Glu Leu Ala
 35 40 45

Lys Lys His Gly Leu Lys Leu His Ile Asp Gly Ala Arg Ile Phe Asn
 50 55 60

Ala Ser Val Ala Leu Gly Val Pro Val Asp Arg Leu Val Gln Ala Ala
 65 70 75 80

Asp Ser Val Ser Val Cys Leu Ser Lys Gly Ile Gly Ala Pro Val Gly
 85 90 95

Ser Val Ile Val Gly Ser Lys Asn Phe Ile Ala Lys Ala Arg Arg Leu
 100 105 110

Arg Lys Thr Leu Gly Gly Gly Met Arg Gln Ile Gly Leu Leu Cys Ala
 115 120 125

Ala Ala Leu Val Ala Leu Gln Glu Asn Val Gly Lys Leu Glu Ser Asp
 130 135 140

His Lys Lys
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<210> 7
 <211> 169
 <212> PRT
 <213> Canola

<220>

<221> misc_feature

<222> (1)..(169)

<223> unknown or other

<400> 7

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Leu	Gly	Val	Pro	Val	His	Arg	Leu	Val	Lys	Ala	Ala	Asp	Ser	Val	Ser	35	40	45	
Val	Cys	Ile	Ser	Lys	Gly	Leu	Gly	Ala	Pro	Val	Gly	Ser	Val	Ile	Val	50	55	60	
Gly	Ser	Thr	Ala	Phe	Ile	Glu	Lys	Ala	Lys	Ile	Leu	Thr	Lys	Thr	Leu	65	70	75	80
Gly	Gly	Gly	Met	Arg	Gln	Val	Gly	Ile	Leu	Cys	Ala	Ala	Ala	Tyr	Val	85	90	95	
Ala	Val	Arg	Asp	Thr	Val	Gly	Lys	Leu	Ala	Asp	Asp	His	Arg	Arg	Ala	100	105	110	
Lys	Val	Leu	Ala	Asp	Gly	Leu	Lys	Lys	Ile	Lys	His	Phe	Arg	Val	Asp	115	120	125	
Thr	Thr	Ser	Val	Glu	Thr	Asn	Met	Val	Phe	Phe	Asp	Ile	Val	Asp	Ser	130	135	140	
Arg	Ile	Ser	Pro	Asp	Lys	Leu	Cys	Gln	Val	Leu	Glu	Gln	Arg	Asn	Val	145	150	155	160
Leu	Ala	Met	Pro	Ala	Gly	Ser	Lys	Arg								165			

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<210> 8
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Ile	Glu	Ile	Lys	Met	Val	Met	Arg	Thr	Val	Asp	Leu	Arg	Ser	Asp	Thr	1	5	10	15
Val	Thr	Arg	Pro	Thr	Asp	Ala	Met	Arg	Glu	Ala	Met	Gly	Ser	Ala	Glu	20	25	30	
Val	Asp	Asp	Asp	Val	Leu	Gly	Tyr	Asp	Pro	Thr	Ala	Arg	Arg	Leu	Glu	35	40	45	
Glu	Glu	Ile	Ala	Lys	Met	Met	Gly	Lys	Glu	Ala	Ala	Leu	Phe	Val	Pro	50	55	60	
Ser	Gly	Thr	Met	Gly	Asn	Leu	Ile	Cys	Val	Met	Val	His	Cys	Asp	Val	65	70	75	80
Arg	Gly	Ser	Glu	Val	Ile	Leu	Gly	Asp	Asn	Cys	His	Ile	His	Val	Tyr	85	90	95	
Glu	Asn	Gly	Gly	Ile	Ser	Thr	Ile	Gly	Gly	Val	His	Pro	Lys	Thr	Ile	100	105	110	
Lys	Asn	Glu	Glu	Asp	Gly	Thr	Met	Asp	Leu	Gly	Ala	Ile	Glu	Ala	Ala	115	120	125	
Ile	Arg	Asp	Pro	Lys	Gly	Ser	Thr	Phe	Tyr	Pro	Ser	Thr	Arg	Leu	Ile	130	135	140	
Cys	Leu	Glu	Asn	Thr	His	Ala	Asn	Ser	Gly	Gly	Arg	Cys	Leu	Ser	Ala	145	150	155	160
Glu	Tyr	Thr	Asp	Arg	Val	Gly	Glu	Ile	Ala	Lys	Arg	His	Gly	Leu	Lys	165	170	175	
Leu	His	Ile	Asp	Gly	Ala	Arg	Leu	Phe	Asn	Ala	Ser	Ile	Ala	Leu	Gly	180	185	190	
Val	Pro	Val	His	Arg	Leu	Val	Gln	Ala	Ala	Asp	Ser	Val	Ser	Val	Cys	195	200	205	
Leu	Ser	Lys	Gly	Leu	Gly	Ala	Pro	Ile	Gly	Ser	Val	Val	Val	Gly	Ser	210	215	220	
Gln	Ser	Phe	Ile	Glu	Lys	Ala	Lys	Thr	Leu	Arg	Lys	Thr	Leu	Gly	Gly	225	230	235	240
Gly	Met	Arg	Gln	Ile	Gly	Val	Leu	Cys	Ala	Ala	Ala	Leu	Val	Ala	Leu	245	250	255	
Gln	Glu	Asn	Leu	Pro	Lys	Leu	Gln	Phe	Asp	His	Lys	Lys	Thr	Lys	Leu	260	265	270	
Leu	Ala	Glu	Gly	Leu	Asn	Gln	Met	Lys	Gly	Ile	Arg	Val	Asn	Val	Ala	275	280	285	

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Ala Met Glu Thr Asn Met Ile Phe Met Asp Met Glu Asp Gly Ser Lys
 290 295 300

Leu Thr Ala Glu Lys Leu Arg Lys Ser Leu Thr Glu His Gly Ile Leu
 305 310 315 320

Val Ile Pro Glu Asn Ser Thr Arg Ile Arg Met Val Leu His His Gln
 325 330 335

Ile Thr Thr Ser Asp Val His Tyr Thr Leu Ser Cys Leu Gln Gln Ala
 340 345 350

Val Gln Thr Ile His Glu Pro Cys Gln Asn
 355 360

<210> 9
 <211> 196
 <212> PRT
 <213> Canola

<400> 9

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 20 25 30

Pro Val Ile Arg Thr Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro
 35 40 45

Thr Glu Ser Met Arg Ser Ala Met Ala Asn Ala Glu Val Asp Asp Asp
 50 55 60

Val Leu Gly Asn Asp Pro Thr Ala Val Leu Leu Glu Arg Glu Val Ala
 65 70 75 80

Glu Ile Ala Gly Lys Glu Ala Ala Met Phe Val Pro Ser Gly Thr Met
 85 90 95

Gly Asn Leu Ile Ser Val Leu Val His Cys Asp Glu Arg Gly Ser Glu
 100 105 110

Val Ile Leu Gly Asp Asp Ser His Ile His Ile Tyr Glu Asn Gly Gly
 115 120 125

Val Ser Ser Leu Gly Gly Val His Pro Arg Thr Val Lys Asn Glu Glu
 130 135 140

Asp Gly Thr Met Glu Ile Ser Ser Ile Glu Ala Ala Val Arg Ser Pro
 145 150 155 160

Thr Gly Asp Leu His Tyr Pro Val Thr Lys Leu Ile Cys Leu Glu Asn
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Thr Gln Ala Asn Cys Gly Gly Arg Cys Leu Pro Ile Glu Tyr Ile Asp
 180 185 190

Lys Val Gly Glu
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<211> 738
<212> DNA
<213> Saccharomyces cerevisiae
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<223> Protein similar to lysine decarboxylase

11

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aag ata gca agg tct acg atg gga cct gat tta agc gga cag gtt cac Lys Ile Ala Arg Ser Thr Met Gly Pro Asp Leu Ser Gly Gln Val His 65 70 75 80	240
ggg atc att cca aat gca ctt gtg tct aag gaa agg aca gac gag gat Gly Ile Ile Pro Asn Ala Leu Val Ser Lys Glu Arg Thr Asp Glu Asp 85 90 95	288
aaa gaa gat gtt aat aaa gca ttg ttg gag tct gta gaa aat cat aag Lys Glu Asp Val Asn Lys Ala Leu Leu Glu Ser Val Glu Asn His Lys 100 105 110	336
ggc gcc act cct att tct gaa gag tat ggg gaa aca acg att gta cca Gly Ala Thr Pro Ile Ser Glu Glu Tyr Gly Glu Thr Thr Ile Val Pro 115 120 125	384
gat atg cat acg aga aaa aga atg atg gca aat ttg agt gac gcg ttt Asp Met His Thr Arg Lys Arg Met Met Ala Asn Leu Ser Asp Ala Phe 130 135 140	432
gtt gct atg cct ggt gga tac ggg act ttt gaa gaa atc atg gaa tgt Val Ala Met Pro Gly Gly Tyr Gly Thr Phe Glu Glu Ile Met Glu Cys 145 150 155 160	480
atc acg tgg tcg caa ctg ggg att cat aat aaa cca att atc ttg ttc Ile Thr Trp Ser Gln Leu Gly Ile His Asn Lys Pro Ile Ile Leu Phe 165 170 175	528
aat atc gat ggg ttc tat gac aaa tta ttg gag ttc ctc aaa cac tct Asn Ile Asp Gly Phe Tyr Asp Lys Leu Leu Glu Phe Leu Lys His Ser 180 185 190	576
att caa gaa cgg ttc atc agt gtg aag aat ggt gaa atc att caa gtt Ile Gln Glu Arg Phe Ile Ser Val Lys Asn Gly Glu Ile Ile Gln Val 195 200 205	624
gcc tcc act ccg cag gaa gtt gtt gat aaa ata gag aag tac gtc gtt Ala Ser Thr Pro Gln Glu Val Val Asp Lys Ile Glu Lys Tyr Val Val 210 215 220	672
cca gag ggc cgt ttc aat ttg aat tgg agc gac gaa ggt cac gct cac Pro Glu Gly Arg Phe Asn Leu Asn Trp Ser Asp Glu Gly His Ala His 225 230 235 240	720
gag gat tgt gct aaa taa Glu Asp Cys Ala Lys 245	738

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 <212> PRT
 <213> *Saccharomyces cerevisiae*

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20 25 30

Ala Leu Tyr Ser Glu Ser Ala Glu Glu Leu Gly Ala Leu Phe His Lys
35 40 45

Leu Gly Trp Lys Leu Val Tyr Gly Gly Gly Thr Thr Gly Leu Met Gly
50 55 60

Lys Ile Ala Arg Ser Thr Met Gly Pro Asp Leu Ser Gly Gln Val His
65 70 75 80

Gly Ile Ile Pro Asn Ala Leu Val Ser Lys Glu Arg Thr Asp Glu Asp
85 90 95

Lys Glu Asp Val Asn Lys Ala Leu Leu Glu Ser Val Glu Asn His Lys
100 105 110

Gly Ala Thr Pro Ile Ser Glu Glu Tyr Gly Glu Thr Thr Ile Val Pro
115 120 125

Asp Met His Thr Arg Lys Arg Met Met Ala Asn Leu Ser Asp Ala Phe
130 135 140

Val Ala Met Pro Gly Gly Tyr Gly Thr Phe Glu Glu Ile Met Glu Cys
145 150 155 160

Ile Thr Trp Ser Gln Leu Gly Ile His Asn Lys Pro Ile Ile Leu Phe
165 170 175

Asn Ile Asp Gly Phe Tyr Asp Lys Leu Leu Glu Phe Leu Lys His Ser
180 185 190

Ile Gln Glu Arg Phe Ile Ser Val Lys Asn Gly Glu Ile Ile Gln Val
195 200 205

Ala Ser Thr Pro Gln Glu Val Val Asp Lys Ile Glu Lys Tyr Val Val
210 215 220

Pro Glu Gly Arg Phe Asn Leu Asn Trp Ser Asp Glu Gly His Ala His
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Glu Asp Cys Ala Lys
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<210> 13
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<212> DNA
<213> Glycine max

<220>

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<223> Threonine aldolase

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1          5          10          15

act gaa gca atg aga gct gct atg gca agt gct gaa gtt gat gac gat      96
Thr Glu Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp
          20          25          30

gtt cta ggc tat gat cca act gct ttt cgc tta gaa aca gag atg gca      144
Val Leu Gly Tyr Asp Pro Thr Ala Phe Arg Leu Glu Thr Glu Met Ala
          35          40          45

aag aca atg ggc aaa gaa gct gct ctt ttt gtt cca tct ggc act atg      192
Lys Thr Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met
          50          55          60

ggg aac ctt gta tct gta ctt gtt cat tgt gat gtc agg gga agt gag      240
Gly Asn Leu Val Ser Val Leu Val His Cys Asp Val Arg Gly Ser Glu
65          70          75          80

gtt att ctt gga gac aat tgc cat atc aac att ttt gag aat gga ggc      288
Val Ile Leu Gly Asp Asn Cys His Ile Asn Ile Phe Glu Asn Gly Gly
          85          90          95

att gca acc att ggg gga gtg cat cca aga caa gtg aaa aat aac gat      336
Ile Ala Thr Ile Gly Gly Val His Pro Arg Gln Val Lys Asn Asn Asp
          100          105          110

gat gga acc atg gac att gat ttg att gag gct gct atc agg gac cca      384
Asp Gly Thr Met Asp Ile Asp Leu Ile Glu Ala Ala Ile Arg Asp Pro
          115          120          125

atg ggg gag cta ttc tat cca acc acc aag ctt att tgc ttg gaa aat      432
Met Gly Glu Leu Phe Tyr Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn
          130          135          140

act cat gca aac tct ggt ggc aga tgc ctc tca gtt gaa tat aca gac      480
Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp
145          150          155          160

aga gtt gga gag tta gct aag aag cat gga ctg aag ctt cac att gat      528
Arg Val Gly Glu Leu Ala Lys Lys His Gly Leu Lys Leu His Ile Asp
          165          170          175

ggg gcc cgt att ttt aac gca tca gtt gca ctt ggt gtt cca gtg gat      576
Gly Ala Arg Ile Phe Asn Ala Ser Val Ala Leu Gly Val Pro Val Asp
          180          185          190

agg ctt gtc cag gcg gct gat tca gtt tcc gtt tgc cta tct aaa ggt      624
Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly
          195          200          205

ata ggt gct cca gtt gga tct gtt att gtt ggt tcc aag aat ttt att      672
Ile Gly Ala Pro Val Gly Ser Val Ile Val Gly Ser Lys Asn Phe Ile
          210          215          220

gcc aag gct aga cga ctc cgg aaa acc tta gga ggt gga atg aga cag      720
Ala Lys Ala Arg Arg Leu Arg Lys Thr Leu Gly Gly Gly Met Arg Gln
225          230          235          240

att ggc ctc ctt tgt gcc gct gca ctt gtt gcc ttg cag gaa aat gtt      768

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Ile Gly Leu Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Val	
245 250 255	
ggg aag ctg gaa agt gat cac aag aaa gct aga ctt ttg gct gat gga	816
Gly Lys Leu Glu Ser Asp His Lys Lys Ala Arg Leu Leu Ala Asp Gly	
260 265 270	
tta aac gaa gtt aaa gga ttg aga gtg gat gcc tgt tct gtg gag acc	864
Leu Asn Glu Val Lys Gly Leu Arg Val Asp Ala Cys Ser Val Glu Thr	
275 280 285	
aat atg gta ttt att gac att gaa gag ggt aca aag act aga gca gaa	912
Asn Met Val Phe Ile Asp Ile Glu Glu Gly Thr Lys Thr Arg Ala Glu	
290 295 300	
aag ata tgc aag tac atg gaa gaa cgt ggt atc ctt gtg atg caa gag	960
Lys Ile Cys Lys Tyr Met Glu Glu Arg Gly Ile Leu Val Met Gln Glu	
305 310 315 320	
agt tca tca aga atg aga gtt gtt ctc cat cac caa ata tca gca agt	1008
Ser Ser Ser Arg Met Arg Val Val Leu His His Gln Ile Ser Ala Ser	
325 330 335	
gat gtg caa tat gcc ttg tcg tgc ttt cag caa gct cta gct gtc aaa	1056
Asp Val Gln Tyr Ala Leu Ser Cys Phe Gln Gln Ala Leu Ala Val Lys	
340 345 350	
gga gta caa aag gaa atg ggc aac taa	1083
Gly Val Gln Lys Glu Met Gly Asn	
355 360	

<210> 14
 <211> 360
 <212> PRT
 <213> Glycine max

<400> 14

Met Val Thr Arg Ile Val Asp Leu Arg Ser Asp Thr Val Thr Lys Pro	
1 5 10 15	
Thr Glu Ala Met Arg Ala Ala Met Ala Ser Ala Glu Val Asp Asp Asp	
20 25 30	
Val Leu Gly Tyr Asp Pro Thr Ala Phe Arg Leu Glu Thr Glu Met Ala	
35 40 45	
Lys Thr Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met	
50 55 60	
Gly Asn Leu Val Ser Val Leu Val His Cys Asp Val Arg Gly Ser Glu	
65 70 75 80	
Val Ile Leu Gly Asp Asn Cys His Ile Asn Ile Phe Glu Asn Gly Gly	
85 90 95	
Ile Ala Thr Ile Gly Gly Val His Pro Arg Gln Val Lys Asn Asn Asp	
100 105 110	

Asp Gly Thr Met Asp Ile Asp Leu Ile Glu Ala Ala Ile Arg Asp Pro
 115 120 125
 Met Gly Glu Leu Phe Tyr Pro Thr Thr Lys Leu Ile Cys Leu Glu Asn
 130 135 140
 Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Val Glu Tyr Thr Asp
 145 150 155 160
 Arg Val Gly Glu Leu Ala Lys Lys His Gly Leu Lys Leu His Ile Asp
 165 170 175
 Gly Ala Arg Ile Phe Asn Ala Ser Val Ala Leu Gly Val Pro Val Asp
 180 185 190
 Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly
 195 200 205
 Ile Gly Ala Pro Val Gly Ser Val Ile Val Gly Ser Lys Asn Phe Ile
 210 215 220
 Ala Lys Ala Arg Arg Leu Arg Lys Thr Leu Gly Gly Gly Met Arg Gln
 225 230 235 240
 Ile Gly Leu Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Val
 245 250 255
 Gly Lys Leu Glu Ser Asp His Lys Lys Ala Arg Leu Leu Ala Asp Gly
 260 265 270
 Leu Asn Glu Val Lys Gly Leu Arg Val Asp Ala Cys Ser Val Glu Thr
 275 280 285
 Asn Met Val Phe Ile Asp Ile Glu Glu Gly Thr Lys Thr Arg Ala Glu
 290 295 300
 Lys Ile Cys Lys Tyr Met Glu Glu Arg Gly Ile Leu Val Met Gln Glu
 305 310 315 320
 Ser Ser Ser Arg Met Arg Val Val Leu His His Gln Ile Ser Ala Ser
 325 330 335
 Asp Val Gln Tyr Ala Leu Ser Cys Phe Gln Gln Ala Leu Ala Val Lys
 340 345 350
 Gly Val Gln Lys Glu Met Gly Asn
 355 360

<210> 15
 <211> 1077
 <212> DNA
 <213> Brassica napus

<220>

<221> CDS

<222> (1) .. (1077)

<223> Threonine aldolase


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<400> 15
atg gtg atg cga act gtg gat cta cgg tca gac acc gtg act aga cct      48
Met Val Met Arg Thr Val Asp Leu Arg Ser Asp Thr Val Thr Arg Pro
1          5          10          15

acc gat gcc atg cgt gaa gca atg gga agc gca gaa gta gac gat gac      96
Thr Asp Ala Met Arg Glu Ala Met Gly Ser Ala Glu Val Asp Asp Asp
          20          25          30

gtc ctc ggc tac gac cca acg gct cga cgt ctt gaa gag gag ata gcc      144
Val Leu Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Glu Ile Ala
          35          40          45

aag atg atg ggg aaa gaa gca gct ctc ttc gtg cca tct ggt aca atg      192
Lys Met Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met
          50          55          60

ggg aac ctc ata tgc gtt atg gtt cac tgc gac gtg aga ggc agc gag      240
Gly Asn Leu Ile Cys Val Met Val His Cys Asp Val Arg Gly Ser Glu
65          70          75          80

gtg att ctt gga gac aac tgt cac atc cat gtc tac gag aac gga ggg      288
Val Ile Leu Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly
          85          90          95

ata tca acg ata gga ggc gtg cat ccc aag aca atc aag aat gaa gaa      336
Ile Ser Thr Ile Gly Gly Val His Pro Lys Thr Ile Lys Asn Glu Glu
          100          105          110

gac ggg aca atg gac ttg ggg gct ata gaa gca gct att aga gat cct      384
Asp Gly Thr Met Asp Leu Gly Ala Ile Glu Ala Ala Ile Arg Asp Pro
          115          120          125

aaa gga agc acg ttt tat cca tca aca agg ttg att tgt ttg gag aac      432
Lys Gly Ser Thr Phe Tyr Pro Ser Thr Arg Leu Ile Cys Leu Glu Asn
          130          135          140

aca cat gcc aac tct ggt ggg aga tgt ttg agt gcg gaa tac aca gat      480
Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Ala Glu Tyr Thr Asp
145          150          155          160

aga gtt gga gag att gcc aag aga cat gga tta aag ctt cat atc gat      528
Arg Val Gly Glu Ile Ala Lys Arg His Gly Leu Lys Leu His Ile Asp
          165          170          175

gga gct cgc ctt ttt aat gct tcc att gca ctt gga gtt cca gtc cat      576
Gly Ala Arg Leu Phe Asn Ala Ser Ile Ala Leu Gly Val Pro Val His
          180          185          190

agg ctt gta cag gct gct gac tct gtt tcg gtg tgt ctc tct aaa ggt      624
Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly
          195          200          205

ctt gga gct cca ata gga tct gta gtc gtt ggt tca cag agt ttc ata      672
Leu Gly Ala Pro Ile Gly Ser Val Val Val Gly Ser Gln Ser Phe Ile
          210          215          220

gaa aag gcg aaa acg tta aga aaa aca tta ggt gga gga atg aga caa      720
Glu Lys Ala Lys Thr Leu Arg Lys Thr Leu Gly Gly Gly Met Arg Gln
225          230          235          240

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ata ggc gtc ctg tgc gca gcc gct ttg gtc gca ctt caa gag aat ctc Ile Gly Val Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Leu 245 250 255	768
cca aag tta caa ttt gac cac aag aag aca aaa ttg tta gct gaa ggg Pro Lys Leu Gln Phe Asp His Lys Lys Thr Lys Leu Leu Ala Glu Gly 260 265 270	816
ttg aat caa atg aaa ggg att aga gtg aac gtt gca gcc atg gag acc Leu Asn Gln Met Lys Gly Ile Arg Val Asn Val Ala Ala Met Glu Thr 275 280 285	864
aac atg ata ttc atg gat atg gag gat gga tca aaa ctg acc gct gaa Asn Met Ile Phe Met Asp Met Glu Asp Gly Ser Lys Leu Thr Ala Glu 290 295 300	912
aaa ctc cgc aag agt cta acg gag cat ggc att ctc gtc atc cct gaa Lys Leu Arg Lys Ser Leu Thr Glu His Gly Ile Leu Val Ile Pro Glu 305 310 315 320	960
aac tct acc cga atc aga atg gtt cta cac cac cag ata aca aca agt Asn Ser Thr Arg Ile Arg Met Val Leu His His Gln Ile Thr Thr Ser 325 330 335	1008
gat gtg cat tac aca ttg tct tgc tta caa caa gca gtg cag acg att Asp Val His Tyr Thr Leu Ser Cys Leu Gln Gln Ala Val Gln Thr Ile 340 345 350	1056
cat gaa cca tgc caa aac taa His Glu Pro Cys Gln Asn 355	1077

<210> 16
 <211> 358
 <212> PRT
 <213> Brassica napus

<400> 16

Met Val Met Arg Thr Val Asp Leu Arg Ser Asp Thr Val Thr Arg Pro 1 5 10 15
Thr Asp Ala Met Arg Glu Ala Met Gly Ser Ala Glu Val Asp Asp Asp 20 25 30
Val Leu Gly Tyr Asp Pro Thr Ala Arg Arg Leu Glu Glu Glu Ile Ala 35 40 45
Lys Met Met Gly Lys Glu Ala Ala Leu Phe Val Pro Ser Gly Thr Met 50 55 60
Gly Asn Leu Ile Cys Val Met Val His Cys Asp Val Arg Gly Ser Glu 65 70 75 80
Val Ile Leu Gly Asp Asn Cys His Ile His Val Tyr Glu Asn Gly Gly 85 90 95
Ile Ser Thr Ile Gly Gly Val His Pro Lys Thr Ile Lys Asn Glu Glu 100 105 110

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Asp Gly Thr Met Asp Leu Gly Ala Ile Glu Ala Ala Ile Arg Asp Pro
 115 120 125
 Lys Gly Ser Thr Phe Tyr Pro Ser Thr Arg Leu Ile Cys Leu Glu Asn
 130 135 140
 Thr His Ala Asn Ser Gly Gly Arg Cys Leu Ser Ala Glu Tyr Thr Asp
 145 150 155 160
 Arg Val Gly Glu Ile Ala Lys Arg His Gly Leu Lys Leu His Ile Asp
 165 170 175
 Gly Ala Arg Leu Phe Asn Ala Ser Ile Ala Leu Gly Val Pro Val His
 180 185 190
 Arg Leu Val Gln Ala Ala Asp Ser Val Ser Val Cys Leu Ser Lys Gly
 195 200 205
 Leu Gly Ala Pro Ile Gly Ser Val Val Val Gly Ser Gln Ser Phe Ile
 210 215 220
 Glu Lys Ala Lys Thr Leu Arg Lys Thr Leu Gly Gly Gly Met Arg Gln
 225 230 235 240
 Ile Gly Val Leu Cys Ala Ala Ala Leu Val Ala Leu Gln Glu Asn Leu
 245 250 255
 Pro Lys Leu Gln Phe Asp His Lys Lys Thr Lys Leu Leu Ala Glu Gly
 260 265 270
 Leu Asn Gln Met Lys Gly Ile Arg Val Asn Val Ala Ala Met Glu Thr
 275 280 285
 Asn Met Ile Phe Met Asp Met Glu Asp Gly Ser Lys Leu Thr Ala Glu
 290 295 300
 Lys Leu Arg Lys Ser Leu Thr Glu His Gly Ile Leu Val Ile Pro Glu
 305 310 315 320
 Asn Ser Thr Arg Ile Arg Met Val Leu His His Gln Ile Thr Thr Ser
 325 330 335
 Asp Val His Tyr Thr Leu Ser Cys Leu Gln Gln Ala Val Gln Thr Ile
 340 345 350
 His Glu Pro Cys Gln Asn
 355

<210> 17
 <211> 570
 <212> DNA
 <213> Glycine max

<220>

<221> CDS

<222> (1)..(570)

<223> Lysine decarboxylase

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<400> 17
atg gaa ata agg gtt tca aag ttc aag agg att tgt gtc ttc tgt ggg      48
Met Glu Ile Arg Val Ser Lys Phe Lys Arg Ile Cys Val Phe Cys Gly
1          5          10          15

agt agc cct ggc aaa aag aga agc tac caa gat gct gcc att gaa ctt      96
Ser Ser Pro Gly Lys Lys Arg Ser Tyr Gln Asp Ala Ala Ile Glu Leu
          20          25          30

ggc aat gaa ttg gtc tca agg aac att gat ctg gtg tat gga ggg gga      144
Gly Asn Glu Leu Val Ser Arg Asn Ile Asp Leu Val Tyr Gly Gly Gly
          35          40          45

agc att ggt cta atg ggt tta gtt tca caa gct gtt cat gat ggc ggt      192
Ser Ile Gly Leu Met Gly Leu Val Ser Gln Ala Val His Asp Gly Gly
          50          55          60

cgg cat gtc atc gga gtt att ccc aag acc ctc atg cct cga gag cta      240
Arg His Val Ile Gly Val Ile Pro Lys Thr Leu Met Pro Arg Glu Leu
65          70          75          80

act ggt gaa aca gtg gga gaa gta aaa gct gtt gct gat atg cac caa      288
Thr Gly Glu Thr Val Gly Glu Val Lys Ala Val Ala Asp Met His Gln
          85          90          95

agg aag gca gag atg gcc aag cat tca gac gcc ttt att gcc tta cca      336
Arg Lys Ala Glu Met Ala Lys His Ser Asp Ala Phe Ile Ala Leu Pro
          100          105          110

ggt gga tat ggg act cta gag gag ctt ctt gaa gtc ata acc tgg gca      384
Gly Gly Tyr Gly Thr Leu Glu Glu Leu Leu Glu Val Ile Thr Trp Ala
          115          120          125

caa ctt ggg att cat gac aag ccg gtg gga tta gta aat gtt gat gga      432
Gln Leu Gly Ile His Asp Lys Pro Val Gly Leu Val Asn Val Asp Gly
          130          135          140

tac ttt aat tcc ttg ctg tca ttt att gac aaa gct gtg gaa gag gga      480
Tyr Phe Asn Ser Leu Leu Ser Phe Ile Asp Lys Ala Val Glu Glu Gly
145          150          155          160

ttt atc agt cca aat gct cgc cac ata att gta tca gca ccc aca gca      528
Phe Ile Ser Pro Asn Ala Arg His Ile Ile Val Ser Ala Pro Thr Ala
          165          170          175

aaa gag ttg gtg aag aaa ttg gag gat tac gtt ccc tgt taa      570
Lys Glu Leu Val Lys Lys Leu Glu Asp Tyr Val Pro Cys
          180          185

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<210> 18
<211> 189
<212> PRT
<213> Glycine max

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<400> 18
Met Glu Ile Arg Val Ser Lys Phe Lys Arg Ile Cys Val Phe Cys Gly
1          5          10          15

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Ser Ser Pro Gly Lys Lys Arg Ser Tyr Gln Asp Ala Ala Ile Glu Leu
20 25 30

Gly Asn Glu Leu Val Ser Arg Asn Ile Asp Leu Val Tyr Gly Gly Gly
35 40 45

Ser Ile Gly Leu Met Gly Leu Val Ser Gln Ala Val His Asp Gly Gly
50 55 60

Arg His Val Ile Gly Val Ile Pro Lys Thr Leu Met Pro Arg Glu Leu
65 70 75 80

Thr Gly Glu Thr Val Gly Glu Val Lys Ala Val Ala Asp Met His Gln
85 90 95

Arg Lys Ala Glu Met Ala Lys His Ser Asp Ala Phe Ile Ala Leu Pro
100 105 110

Gly Gly Tyr Gly Thr Leu Glu Glu Leu Leu Glu Val Ile Thr Trp Ala
115 120 125

Gln Leu Gly Ile His Asp Lys Pro Val Gly Leu Val Asn Val Asp Gly
130 135 140

Tyr Phe Asn Ser Leu Leu Ser Phe Ile Asp Lys Ala Val Glu Glu Gly
145 150 155 160

Phe Ile Ser Pro Asn Ala Arg His Ile Ile Val Ser Ala Pro Thr Ala
165 170 175

Lys Glu Leu Val Lys Lys Leu Glu Asp Tyr Val Pro Cys
180 185

<210> 19
<211> 675
<212> DNA
<213> Hordeum vulgare

<220>

<221> CDS

<222> (1)..(675)

<223> Lysine decarboxylase

<400> 19
atg ggc gac acc acc gcg ccc tcg ccg ccg agg agg ttc ggc agg atc 48
Met Gly Asp Thr Thr Ala Pro Ser Pro Pro Arg Arg Phe Gly Arg Ile
1 5 10 15

tgc gtc ttc tgc ggc agg aac tcc ggc aac cgc gcc gtg ttc ggc gac 96
Cys Val Phe Cys Gly Arg Asn Ser Gly Asn Arg Ala Val Phe Gly Asp
20 25 30

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gcc gcg ctc gag ctc ggc cag ggc ctg gtg acg agg ggg gtc gat ctg Ala Ala Leu Glu Leu Gly Gln Gly Leu Val Thr Arg Gly Val Asp Leu 35 40 45	144
gtc tac ggc ggc ggc agt atc ggg ctg atg ggc ctg atc gcg cag acg Val Tyr Gly Gly Gly Ser Ile Gly Leu Met Gly Leu Ile Ala Gln Thr 50 55 60	192
gtt ctc gac ggc ggc tgc cgc gtc ctc ggg gtg att cca aga gca ctc Val Leu Asp Gly Gly Cys Arg Val Leu Gly Val Ile Pro Arg Ala Leu 65 70 75 80	240
atg ccc ctc gag ata tcc ggt gca agt gtt gga gaa gta aag att gtc Met Pro Leu Glu Ile Ser Gly Ala Ser Val Gly Glu Val Lys Ile Val 85 90 95	288
tcc gac atg cat gag agg aaa gct gag atg gcg cga caa gcc gat gca Ser Asp Met His Glu Arg Lys Ala Glu Met Ala Arg Gln Ala Asp Ala 100 105 110	336
ttc att gct ctt ccg ggt ggg tat gga aca atg gaa gag ctg gta gag Phe Ile Ala Leu Pro Gly Gly Tyr Gly Thr Met Glu Glu Leu Val Glu 115 120 125	384
atg atc act tgg tcg cag ctt gga atc cat gac aaa ccg gtc ggg ttg Met Ile Thr Trp Ser Gln Leu Gly Ile His Asp Lys Pro Val Gly Leu 130 135 140	432
cta aac gtc gat ggg tac tat gat ccg tta ctc gcg ctg ttc gac aag Leu Asn Val Asp Gly Tyr Tyr Asp Pro Leu Leu Ala Leu Phe Asp Lys 145 150 155 160	480
ggc gcg ggg gaa ggg ttt ttt aag gcc gat tgc agg ccg ata atc gtg Gly Ala Gly Glu Gly Phe Phe Lys Ala Asp Cys Arg Pro Ile Ile Val 165 170 175	528
tcg gca cca act gcc cac gaa ctg ctg aca aaa atg gag caa tac acc Ser Ala Pro Thr Ala His Glu Leu Leu Thr Lys Met Glu Gln Tyr Thr 180 185 190	576
cgt tca ccc cgg gag gtg gcc tcg cgg acg agc tgg gag atg acc gag Arg Ser Pro Arg Glu Val Ala Ser Arg Thr Ser Trp Glu Met Thr Glu 195 200 205	624
atg ggc tcc ggg aaa gca ccg gag ccg gag gag gag gcg gcg gca tcg Met Gly Ser Gly Lys Ala Pro Glu Pro Glu Glu Glu Ala Ala Ala Ser 210 215 220	672
taa	675
 <210> 20 <211> 224 <212> PRT <213> Hordeum vulgare	
 <400> 20	
Met Gly Asp Thr Thr Ala Pro Ser Pro Pro Arg Arg Phe Gly Arg Ile 1 5 10 15	

Cys Val Phe Cys Gly Arg Asn Ser Gly Asn Arg Ala Val Phe Gly Asp
20 25 30

Ala Ala Leu Glu Leu Gly Gln Gly Leu Val Thr Arg Gly Val Asp Leu
35 40 45

Val Tyr Gly Gly Gly Ser Ile Gly Leu Met Gly Leu Ile Ala Gln Thr
50 55 60

Val Leu Asp Gly Gly Cys Arg Val Leu Gly Val Ile Pro Arg Ala Leu
65 70 75 80

Met Pro Leu Glu Ile Ser Gly Ala Ser Val Gly Glu Val Lys Ile Val
85 90 95

Ser Asp Met His Glu Arg Lys Ala Glu Met Ala Arg Gln Ala Asp Ala
100 105 110

Phe Ile Ala Leu Pro Gly Gly Tyr Gly Thr Met Glu Glu Leu Val Glu
115 120 125

Met Ile Thr Trp Ser Gln Leu Gly Ile His Asp Lys Pro Val Gly Leu
130 135 140

Leu Asn Val Asp Gly Tyr Tyr Asp Pro Leu Leu Ala Leu Phe Asp Lys
145 150 155 160

Gly Ala Gly Glu Gly Phe Phe Lys Ala Asp Cys Arg Pro Ile Ile Val
165 170 175

Ser Ala Pro Thr Ala His Glu Leu Leu Thr Lys Met Glu Gln Tyr Thr
180 185 190

Arg Ser Pro Arg Glu Val Ala Ser Arg Thr Ser Trp Glu Met Thr Glu
195 200 205

Met Gly Ser Gly Lys Ala Pro Glu Pro Glu Glu Glu Ala Ala Ala Ser
210 215 220

<210> 21
<211> 717
<212> DNA
<213> artificial

<220>

<221> CDS

<222> (1)..(717)

<223> Lysine decarboxylase

<400> 21

atg gag gag aat caa gag aag ttt gct ccg gag agc agc ggc ggc gac
Met Glu Glu Asn Gln Glu Lys Phe Ala Pro Glu Ser Ser Gly Gly Thr
1 5 10 15

48

ggt ggt ggc tgc gtg aga acg atc tgc gtc ttc tgc ggc agc agg ccg Gly Gly Gly Ser Val Arg Thr Ile Cys Val Phe Cys Gly Ser Arg Pro 20 25 30	96
ggg aac cgg ccg tcc ttc agc gct gcg gcg ctc gac ctg ggg aag cag Gly Asn Arg Pro Ser Phe Ser Ala Ala Ala Leu Asp Leu Gly Lys Gln 35 40 45	144
ctg gtc gag agg cag atg aac ctg gtg tac ggc ggc ggc agc ggc ggg Leu Val Glu Arg Gln Met Asn Leu Val Tyr Gly Gly Gly Ser Gly Gly 50 55 60	192
ctg atg ggc ctg gtg tcc aag gcc gtc tac gaa ggc ggc cgc cac gtc Leu Met Gly Leu Val Ser Lys Ala Val Tyr Glu Gly Gly Arg His Val 65 70 75 80	240
ctc ggg gtc atc cct acc gcc ctc cta cct gaa gag gtg tca ggg gag Leu Gly Val Ile Pro Thr Ala Leu Leu Pro Glu Glu Val Ser Gly Glu 85 90 95	288
aca ttg gga gag gtg aaa gtg gtc agg gac atg cat cag cgc aag gcg Thr Leu Gly Glu Val Lys Val Val Arg Asp Met His Gln Arg Lys Ala 100 105 110	336
gaa atg gcg aaa cat gcc gac gct ttc atc gcc ctg cca ggt ggt tac Glu Met Ala Lys His Ala Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr 115 120 125	384
ggg aca atc gaa gaa ctg ctg gag atc ata gcg tgg gcg cag ctg ggc Gly Thr Ile Glu Glu Leu Leu Glu Ile Ile Ala Trp Ala Gln Leu Gly 130 135 140	432
atc cac agc aaa ccg gtg ggg ttg ctc aac gtg gac ggc tac tac aac Ile His Ser Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asn 145 150 155 160	480
agc ctg ctc tgc ctg ttc gac aag gct gtc gag gag ggc ttc atc gac Ser Leu Leu Ser Leu Phe Asp Lys Ala Val Glu Glu Gly Phe Ile Asp 165 170 175	528
acc aag gca cgg aac atc ttc gtc ctc gct gac acc gcc gcc gac ctg Thr Lys Ala Arg Asn Ile Phe Val Leu Ala Asp Thr Ala Ala Asp Leu 180 185 190	576
ctg act agg ctc acc atg atg gcg cgc ctg gca gcc gac gac gac gat Leu Thr Arg Leu Thr Met Met Ala Arg Leu Ala Ala Asp Asp Asp Asp 195 200 205	624
gct act act acc ccc aga gga gac gga gac gga gac gga gac gaa cac Ala Thr Thr Thr Pro Arg Gly Asp Gly Asp Gly Asp Gly Asp Glu His 210 215 220	672
aag ggg gcc acc acc gct gca ggc gtc aaa agg aaa agg ggc taa Lys Gly Ala Thr Thr Ala Ala Gly Val Lys Arg Lys Arg Gly 225 230 235	717

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<210> 22
 <211> 238
 <212> PRT
 <213> artificial

<400> 22

Met Glu Glu Asn Gln Glu Lys Phe Ala Pro Glu Ser Ser Gly Gly Asp
 1 5 10 15
 Gly Gly Gly Ser Val Arg Thr Ile Cys Val Phe Cys Gly Ser Arg Pro
 20 25 30
 Gly Asn Arg Pro Ser Phe Ser Ala Ala Ala Leu Asp Leu Gly Lys Gln
 35 40 45
 Leu Val Glu Arg Gln Met Asn Leu Val Tyr Gly Gly Gly Ser Gly Gly
 50 55 60
 Leu Met Gly Leu Val Ser Lys Ala Val Tyr Glu Gly Gly Arg His Val
 65 70 75 80
 Leu Gly Val Ile Pro Thr Ala Leu Leu Pro Glu Glu Val Ser Gly Glu
 85 90 95
 Thr Leu Gly Glu Val Lys Val Val Arg Asp Met His Gln Arg Lys Ala
 100 105 110
 Glu Met Ala Lys His Ala Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr
 115 120 125
 Gly Thr Ile Glu Glu Leu Leu Glu Ile Ile Ala Trp Ala Gln Leu Gly
 130 135 140
 Ile His Ser Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asn
 145 150 155 160
 Ser Leu Leu Ser Leu Phe Asp Lys Ala Val Glu Glu Gly Phe Ile Asp
 165 170 175
 Thr Lys Ala Arg Asn Ile Phe Val Leu Ala Asp Thr Ala Ala Asp Leu
 180 185 190
 Leu Thr Arg Leu Thr Met Met Ala Arg Leu Ala Ala Asp Asp Asp Asp
 195 200 205
 Ala Thr Thr Thr Pro Arg Gly Asp Gly Asp Gly Asp Gly Asp Glu His
 210 215 220
 Lys Gly Ala Thr Thr Ala Ala Gly Val Lys Arg Lys Arg Gly
 225 230 235

<210> 23
 <211> 717
 <212> DNA
 <213> Zea mays

PF 54195

<220>

<221> CDS

<222> (1)..(717)

<223> Lysine decarboxylase

<400> 23

atg gag gag aat caa gag aag ttt gct ccg gag agc agc ggc ggc gac	48
Met Glu Glu Asn Gln Glu Lys Phe Ala Pro Glu Ser Ser Gly Gly Asp	
1 5 10 15	
ggg ggt ggc tgc gtg aga acg atc tgc gtc ttc tgc ggc agc agg ccg	96
Gly Gly Gly Ser Val Arg Thr Ile Cys Val Phe Cys Gly Ser Arg Pro	
20 25 30	
ggg aac cgg ccg tcc ttc agc gct gcg gcg ctc gac ctg ggg aag cag	144
Gly Asn Arg Pro Ser Phe Ser Ala Ala Ala Leu Asp Leu Gly Lys Gln	
35 40 45	
ctg gtc gag agg cag atg aac ctg gtg tac ggc ggc ggc agc ggc ggc	192
Leu Val Glu Arg Gln Met Asn Leu Val Tyr Gly Gly Gly Ser Gly Gly	
50 55 60	
ctg atg ggc ctg gtg tcc aag gcc gtc tac gaa ggc ggc cgc cac gtc	240
Leu Met Gly Leu Val Ser Lys Ala Val Tyr Glu Gly Gly Arg His Val	
65 70 75 80	
ctc ggg gtc atc cct acc gcc ctc cta cct gaa gag gtg tca ggg gag	288
Leu Gly Val Ile Pro Thr Ala Leu Leu Pro Glu Glu Val Ser Gly Glu	
85 90 95	
aca ttg gga gag gtg aaa gtg gtc agg gac atg cat cag cgc aag gcg	336
Thr Leu Gly Glu Val Lys Val Val Arg Asp Met His Gln Arg Lys Ala	
100 105 110	
gaa atg gcg aaa cat gcc gac gct ttc atc gcc ctg cca ggt ggt tac	384
Glu Met Ala Lys His Ala Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr	
115 120 125	
ggg aca atc gaa gaa ctg ctg gag atc ata gcg tgg gcg cag ctg ggc	432
Gly Thr Ile Glu Glu Leu Glu Ile Ile Ala Trp Ala Gln Leu Gly	
130 135 140	
atc cac agc aaa ccg gtg ggg ttg ctc aac gtg gac ggc tac tac aac	480
Ile His Ser Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asn	
145 150 155 160	
agc ctg ctc tgc ctg ttc gac aag gct gtc gag gag ggc ttc atc gac	528
Ser Leu Leu Ser Leu Phe Asp Lys Ala Val Glu Glu Gly Phe Ile Asp	
165 170 175	
acc aag gca cgg aac atc ttc gtc ctc gct gac acc gcc gcc gac ctg	576
Thr Lys Ala Arg Asn Ile Phe Val Leu Ala Asp Thr Ala Ala Asp Leu	
180 185 190	
ctg act agg ctc acc atg atg gcg cgc ctg gca gcc gac gac gac gat	624
Leu Thr Arg Leu Thr Met Met Ala Arg Leu Ala Ala Asp Asp Asp Asp	
195 200 205	

gct act act acc ccc aga gga gac gga gac gga gac gga gac gaa cac 672
Ala Thr Thr Thr Pro Arg Gly Asp Gly Asp Gly Asp Gly Asp Glu His
210 215 220

aag ggg gcc acc acc gct gca ggc gtc aaa agg aaa agg ggc taa 717
Lys Gly Ala Thr Thr Ala Ala Gly Val Lys Arg Lys Arg Gly
225 230 235

<210> 24
<211> 238
<212> PRT
<213> Zea mays

<400> 24

Met Glu Glu Asn Gln Glu Lys Phe Ala Pro Glu Ser Ser Gly Gly Asp
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Gly Gly Gly Ser Val Arg Thr Ile Cys Val Phe Cys Gly Ser Arg Pro
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Gly Asn Arg Pro Ser Phe Ser Ala Ala Ala Leu Asp Leu Gly Lys Gln
35 40 45
Leu Val Glu Arg Gln Met Asn Leu Val Tyr Gly Gly Gly Ser Gly Gly
50 55 60
Leu Met Gly Leu Val Ser Lys Ala Val Tyr Glu Gly Gly Arg His Val
65 70 75 80
Leu Gly Val Ile Pro Thr Ala Leu Leu Pro Glu Glu Val Ser Gly Glu
85 90 95
Thr Leu Gly Glu Val Lys Val Val Arg Asp Met His Gln Arg Lys Ala
100 105 110
Glu Met Ala Lys His Ala Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr
115 120 125
Gly Thr Ile Glu Glu Leu Leu Glu Ile Ile Ala Trp Ala Gln Leu Gly
130 135 140
Ile His Ser Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asn
145 150 155 160
Ser Leu Leu Ser Leu Phe Asp Lys Ala Val Glu Glu Gly Phe Ile Asp
165 170 175
Thr Lys Ala Arg Asn Ile Phe Val Leu Ala Asp Thr Ala Ala Asp Leu
180 185 190
Leu Thr Arg Leu Thr Met Met Ala Arg Leu Ala Ala Asp Asp Asp Asp
195 200 205
Ala Thr Thr Thr Pro Arg Gly Asp Gly Asp Gly Asp Gly Asp Glu His
210 215 220
Lys Gly Ala Thr Thr Ala Ala Gly Val Lys Arg Lys Arg Gly
225 230 235

PF 54195

<210> 25
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 <212> DNA
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<220>

<221> CDS

<222> (1)..(672)

<223> Lysine decarboxylase

<400> 25
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 agg ttc ggc agg atc tgc gtc ttc tgc ggc agc aac gcc ggc aac cgc 96
 Arg Phe Gly Arg Ile Cys Val Phe Cys Gly Ser Asn Ala Gly Asn Arg
 20 25 30
 gcg gtg ttc ggc gac gcg gcg ctc cag ctc ggg cag gag ctg gtg tcg 144
 Ala Val Phe Gly Asp Ala Ala Leu Gln Leu Gly Gln Glu Leu Val Ser
 35 40 45
 aga ggg atc gag ttg gtc tac ggt ggc ggc agc gtc ggg ttg atg ggc 192
 Arg Gly Ile Glu Leu Val Tyr Gly Gly Gly Ser Val Gly Leu Met Gly
 50 55 60
 ttg atc gcg cag acg gtt ctt gat ggc ggc tgc ggt gtt ctc ggg gtg 240
 Leu Ile Ala Gln Thr Val Leu Asp Gly Gly Cys Gly Val Leu Gly Val
 65 70 75 80
 att cca aaa gca ctt atg ccc acc gag ata tca ggt gca agt gtt gga 288
 Ile Pro Lys Ala Leu Met Pro Thr Glu Ile Ser Gly Ala Ser Val Gly
 85 90 95
 gaa gtg aaa att gtg tct gac atg cat gag agg aaa gct gag atg gca 336
 Glu Val Lys Ile Val Ser Asp Met His Glu Arg Lys Ala Glu Met Ala
 100 105 110
 cgc caa tcc gat gcc ttc atc gct ctt cct gga ggg tat gga aca atg 384
 Arg Gln Ser Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr Gly Thr Met
 115 120 125
 gag gag ttg tta gag atg ata act tgg tca caa ctt gga att cat gac 432
 Glu Glu Leu Leu Glu Met Ile Thr Trp Ser Gln Leu Gly Ile His Asp
 130 135 140
 aaa cca gtt ggg ttg ctg aat gtg gac ggt tac tat gat ccg ttg ctt 480
 Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asp Pro Leu Leu
 145 150 155 160
 gcg cta ttt gat aag ggt gcg gca gaa gga ttt att aag gcc gat tgc 528
 Ala Leu Phe Asp Lys Gly Ala Ala Glu Gly Phe Ile Lys Ala Asp Cys
 165 170 175

aga caa ata att gtt tcg gca ccg act gcg cat gag ctg ctg aga aag 576
 Arg Gln Ile Ile Val Ser Ala Pro Thr Ala His Glu Leu Leu Arg Lys
 180 185 190

atg gag caa tac act cgt tca cac cag gag gta gcg cca cgt aca agc 624
 Met Glu Gln Tyr Thr Arg Ser His Gln Glu Val Ala Pro Arg Thr Ser
 195 200 205

tgg gag atg tca gag ctt ggt tat gga aag aca cca gag gaa tcg taa 672
 Trp Glu Met Ser Glu Leu Gly Tyr Gly Lys Thr Pro Glu Glu Ser
 210 215 220

<210> 26
 <211> 223
 <212> PRT
 <213> Oryza sativa

<400> 26

Met Gly Asp Asn Ser Ala Ala Ala Ala Ala Val Ala Ala Pro Arg Gly
 1 5 10 15
 Arg Phe Gly Arg Ile Cys Val Phe Cys Gly Ser Asn Ala Gly Asn Arg
 20 25 30
 Ala Val Phe Gly Asp Ala Ala Leu Gln Leu Gly Gln Glu Leu Val Ser
 35 40 45
 Arg Gly Ile Glu Leu Val Tyr Gly Gly Gly Ser Val Gly Leu Met Gly
 50 55 60
 Leu Ile Ala Gln Thr Val Leu Asp Gly Gly Cys Gly Val Leu Gly Val
 65 70 75 80
 Ile Pro Lys Ala Leu Met Pro Thr Glu Ile Ser Gly Ala Ser Val Gly
 85 90 95
 Glu Val Lys Ile Val Ser Asp Met His Glu Arg Lys Ala Glu Met Ala
 100 105 110
 Arg Gln Ser Asp Ala Phe Ile Ala Leu Pro Gly Gly Tyr Gly Thr Met
 115 120 125
 Glu Glu Leu Leu Glu Met Ile Thr Trp Ser Gln Leu Gly Ile His Asp
 130 135 140
 Lys Pro Val Gly Leu Leu Asn Val Asp Gly Tyr Tyr Asp Pro Leu Leu
 145 150 155 160
 Ala Leu Phe Asp Lys Gly Ala Ala Glu Gly Phe Ile Lys Ala Asp Cys
 165 170 175
 Arg Gln Ile Ile Val Ser Ala Pro Thr Ala His Glu Leu Leu Arg Lys
 180 185 190
 Met Glu Gln Tyr Thr Arg Ser His Gln Glu Val Ala Pro Arg Thr Ser
 195 200 205
 Trp Glu Met Ser Glu Leu Gly Tyr Gly Lys Thr Pro Glu Glu Ser
 210 215 220